

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals

<120> Novel Compounds

<130> BM45324

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2442

<212> DNA

<213> Bacteria

<400> 1

atgcgtaatt	catatttttaa	aggtttttcag	gtcagtgcaa	tgacaatggc	tgtcatgatg	60
gtaatgtcaa	ctcatgcaca	agcggcggat	tttatggcaa	atgacattac	catcacagga	120
ctacagcgag	tgaccattga	aagcttacaa	agcgtgctgc	cgtttcgtct	gggtcaagtg	180
gtgagcgaaa	accagttggc	tgatggtgtc	aaagcacttt	atgcaacagg	caatttttca	240
gatgtgcaag	tctatcatca	agaaggcggt	atcatctatc	aggtaaccga	aaggccggtta	300
atcgctgaga	ttaattttga	gggcaatcgc	ttaattccaa	aagaagggtct	acaagaaggg	360
ctaaaaaatg	ctggcttagc	tgtgggtcaa	ccactaaaac	aagccacagt	acagatgatc	420
gaaaccgagc	ttaccaatca	atatatatca	caaggctatt	ataataccga	aattactgtc	480
aaacagacga	tgcttgatgg	taatcgtgtt	aagcttgata	tgacctttgc	tgaaggtaaa	540
cctgcacggg	tgggtgatat	taatatcatt	ggcaatcagc	atttttagcga	tgagatattg	600
attgatgtgc	ttgcgattaa	ggataataaa	atcaatccac	tgtctaaagc	tgaccgttat	660
actcaagaaa	agctgggtgac	cagtttagag	aatttgctgt	ctaaatatct	caatgcaggg	720
tttgtgcgtt	ttgagattaa	agatgctaag	cttaatatata	atgaagataa	aaaccgtatc	780
tttgttgaga	tttcattgca	tgaagggtgag	caatatcgct	ttggacagac	acagtttttg	840
ggtaatttaa	cttatactca	agcagaactt	gaggcactgc	ttaaattcaa	agcagaagaa	900
gggttttcac	aagccatgct	tgagcaaaca	acaaacaata	tcagtaccaa	atttgggtgac	960
gatggctatt	attatgtcca	aatccgtcct	gtaacacgca	ttaatgatga	aagtcgtacg	1020
gttgatgtgg	aatattatat	tgaccctgta	caccctgtct	atgtacgccg	tattaatattt	1080
acaggtaact	ttaagaccca	agatgaagta	ctccgtcgtg	agatgcgaca	acttgaaggt	1140
gcgttggcat	ctaatacaaaa	aatccagctg	tctcgtgcac	gcttgatgcg	gactgggttt	1200
tttaaacatg	ttaccgttga	tactcgtcca	gtacccaact	cacctgatca	ggttgatgta	1260
aattttgtgg	ttgaagaaca	accttcagga	tcatcaacca	tcgcagcagg	ctactctcaa	1320
agtgggtggg	taacttttca	atttgatgtt	tctcaaaaata	actttatggg	tacaggtaag	1380
cacgtcaatg	cttcgttttc	tcgctctgag	acccgtgagg	tgtatagttt	gggtatgacc	1440
aaccatact	ttaccgtaaa	tggcgtctcg	caaagcttga	gtggctacta	tcgtaaaacc	1500
aagtatgata	acaagaacat	tagtaattat	gtacttgatt	cttatgggtg	ctcattaagc	1560
tatggatata	caattgatga	aaatcaacgc	ataagctttg	gtctgaatgc	tgacaatacc	1620
aagcttcatg	gcggtcgttt	tatgggcatt	agtaatgtca	agcagctgat	ggcagatggt	1680
ggcaaaaattc	aagtggataa	taatggcatt	cctgatttta	agcatgatta	cacaacctac	1740
aatgccattt	tgggggtggaa	ttattcaagt	ctagatcgcc	ctgtatttcc	aaccgaaggc	1800
atgagtcatt	ctgtagattt	gacgggtggg	tttgggtgata	aaactcatca	aaaagtgggt	1860
tatcaaggca	atatctatcg	cccattttatc	aaaaaatcag	tcttgcgtgg	atacgccaag	1920
ttaggctatg	gcaataattt	accatttttat	gaaaatttct	atgcaggcgg	ctatggttcg	1980
gttcgtggct	atgatcaatc	ctctttgggt	ccacgctcac	aagcctattt	gacagctcgt	2040
cgtgggtcaac	aaaccacact	aggagaggtt	gttgggtgga	atgctttggc	aactttcggc	2100
agtgagctga	ttttaccttt	gccattttaa	ggtgattgga	tagatcaggt	gcgtccagtg	2160
atattcattg	agggcggtca	ggtttttgat	acaacaggta	tggataaaca	aaccattgat	2220
ttaacccaat	ttaaagaccc	acaagcaaca	gctgaacaaa	atgcaaaagc	agccaatcgc	2280
ccgctactaa	cccaagataa	acagttgcgt	tatagtgcgt	gtgttgggtg	aacttgggtat	2340

acgcccattg gtcctttatc tattagctat gccaaagccat tgaataaaaa acaaaatgat 2400
cagaccgata cggtagagtt ccagattggg agtgtctttt aa 2442

<210> 2
<211> 813
<212> PRT
<213> Bacteria

<400> 2
Met Arg Asn Ser Tyr Phe Lys Gly Phe Gln Val Ser Ala Met Thr Met
1 5 10 15
Ala Val Met Met Val Met Ser Thr His Ala Gln Ala Ala Asp Phe Met
20 25 30
Ala Asn Asp Ile Thr Ile Thr Gly Leu Gln Arg Val Thr Ile Glu Ser
35 40 45
Leu Gln Ser Val Leu Pro Phe Arg Leu Gly Gln Val Val Ser Glu Asn
50 55 60
Gln Leu Ala Asp Gly Val Lys Ala Leu Tyr Ala Thr Gly Asn Phe Ser
65 70 75 80
Asp Val Gln Val Tyr His Gln Glu Gly Arg Ile Ile Tyr Gln Val Thr
85 90 95
Glu Arg Pro Leu Ile Ala Glu Ile Asn Phe Glu Gly Asn Arg Leu Ile
100 105 110
Pro Lys Glu Gly Leu Gln Glu Gly Leu Lys Asn Ala Gly Leu Ala Val
115 120 125
Gly Gln Pro Leu Lys Gln Ala Thr Val Gln Met Ile Glu Thr Glu Leu
130 135 140
Thr Asn Gln Tyr Ile Ser Gln Gly Tyr Tyr Asn Thr Glu Ile Thr Val
145 150 155 160
Lys Gln Thr Met Leu Asp Gly Asn Arg Val Lys Leu Asp Met Thr Phe
165 170 175
Ala Glu Gly Lys Pro Ala Arg Val Val Asp Ile Asn Ile Ile Gly Asn
180 185 190
Gln His Phe Ser Asp Ala Asp Leu Ile Asp Val Leu Ala Ile Lys Asp
195 200 205
Asn Lys Ile Asn Pro Leu Ser Lys Ala Asp Arg Tyr Thr Gln Glu Lys
210 215 220
Leu Val Thr Ser Leu Glu Asn Leu Arg Ala Lys Tyr Leu Asn Ala Gly
225 230 235 240
Phe Val Arg Phe Glu Ile Lys Asp Ala Lys Leu Asn Ile Asn Glu Asp
245 250 255
Lys Asn Arg Ile Phe Val Glu Ile Ser Leu His Glu Gly Glu Gln Tyr
260 265 270
Arg Phe Gly Gln Thr Gln Phe Leu Gly Asn Leu Thr Tyr Thr Gln Ala
275 280 285
Glu Leu Glu Ala Leu Leu Lys Phe Lys Ala Glu Glu Gly Phe Ser Gln
290 295 300
Ala Met Leu Glu Gln Thr Thr Asn Asn Ile Ser Thr Lys Phe Gly Asp
305 310 315 320
Asp Gly Tyr Tyr Tyr Ala Gln Ile Arg Pro Val Thr Arg Ile Asn Asp
325 330 335
Glu Ser Arg Thr Val Asp Val Glu Tyr Tyr Ile Asp Pro Val His Pro
340 345 350
Val Tyr Val Arg Arg Ile Asn Phe Thr Gly Asn Phe Lys Thr Gln Asp
355 360 365
Glu Val Leu Arg Arg Glu Met Arg Gln Leu Glu Gly Ala Leu Ala Ser
370 375 380
Asn Gln Lys Ile Gln Leu Ser Arg Ala Arg Leu Met Arg Thr Gly Phe

```

385          390          395          400
Phe Lys His Val Thr Val Asp Thr Arg Pro Val Pro Asn Ser Pro Asp
          405          410          415
Gln Val Asp Val Asn Phe Val Val Glu Glu Gln Pro Ser Gly Ser Ser
          420          425          430
Thr Ile Ala Ala Gly Tyr Ser Gln Ser Gly Gly Val Thr Phe Gln Phe
          435          440          445
Asp Val Ser Gln Asn Asn Phe Met Gly Thr Gly Lys His Val Asn Ala
          450          455          460
Ser Phe Ser Arg Ser Glu Thr Arg Glu Val Tyr Ser Leu Gly Met Thr
          465          470          475          480
Asn Pro Tyr Phe Thr Val Asn Gly Val Ser Gln Ser Leu Ser Gly Tyr
          485          490          495
Tyr Arg Lys Thr Lys Tyr Asp Asn Lys Asn Ile Ser Asn Tyr Val Leu
          500          505          510
Asp Ser Tyr Gly Gly Ser Leu Ser Tyr Gly Tyr Pro Ile Asp Glu Asn
          515          520          525
Gln Arg Ile Ser Phe Gly Leu Asn Ala Asp Asn Thr Lys Leu His Gly
          530          535          540
Gly Arg Phe Met Gly Ile Ser Asn Val Lys Gln Leu Met Ala Asp Gly
          545          550          555          560
Gly Lys Ile Gln Val Asp Asn Asn Gly Ile Pro Asp Phe Lys His Asp
          565          570          575
Tyr Thr Thr Tyr Asn Ala Ile Leu Gly Trp Asn Tyr Ser Ser Leu Asp
          580          585          590
Arg Pro Val Phe Pro Thr Gln Gly Met Ser His Ser Val Asp Leu Thr
          595          600          605
Val Gly Phe Gly Asp Lys Thr His Gln Lys Val Val Tyr Gln Gly Asn
          610          615          620
Ile Tyr Arg Pro Phe Ile Lys Lys Ser Val Leu Arg Gly Tyr Ala Lys
          625          630          635          640
Leu Gly Tyr Gly Asn Asn Leu Pro Phe Tyr Glu Asn Phe Tyr Ala Gly
          645          650          655
Gly Tyr Gly Ser Val Arg Gly Tyr Asp Gln Ser Ser Leu Gly Pro Arg
          660          665          670
Ser Gln Ala Tyr Leu Thr Ala Arg Arg Gly Gln Gln Thr Thr Leu Gly
          675          680          685
Glu Val Val Gly Gly Asn Ala Leu Ala Thr Phe Gly Ser Glu Leu Ile
          690          695          700
Leu Pro Leu Pro Phe Lys Gly Asp Trp Ile Asp Gln Val Arg Pro Val
          705          710          715          720
Ile Phe Ile Glu Gly Gly Gln Val Phe Asp Thr Thr Gly Met Asp Lys
          725          730          735
Gln Thr Ile Asp Leu Thr Gln Phe Lys Asp Pro Gln Ala Thr Ala Glu
          740          745          750
Gln Asn Ala Lys Ala Ala Asn Arg Pro Leu Leu Thr Gln Asp Lys Gln
          755          760          765
Leu Arg Tyr Ser Ala Gly Val Gly Ala Thr Trp Tyr Thr Pro Ile Gly
          770          775          780
Pro Leu Ser Ile Ser Tyr Ala Lys Pro Leu Asn Lys Lys Gln Asn Asp
          785          790          795          800
Gln Thr Asp Thr Val Gln Phe Gln Ile Gly Ser Val Phe
          805          810

```

```

<210> 3
<211> 2442
<212> DNA
<213> Bacteria

```

<400> 3

```

atgcgtaatt catattttaa aggttttcag gtcagtgc aa tgacaatggc tgtcatgatg      60
gtaatgtcaa ctcatgcaca agcggcgcat ttatggcaa atgacattgc catcacagga      120
ctacagcgag tgaccattga aagcttacaa agcgtgctgc cgtttcgcct gggtaagtg      180
gtgagcgaag cacagttggc tgatgggtgc aaagcacttt atgcaacagg caatttttca      240
gatgtgcaag tctatcatca agaagggcgt atcatctatc aggtaaccca aaggccggtta      300
atcgtcgaga ttaattttga gggcaatcgc ttaattccaa aagaaggtct acaagaaggg      360
ctaaaaaatg ctggcttagc tgtgggtcaa ccactaaaac aagccacagt acagatgatc      420
gaaaccgagc ttaccaatca atatatatca caaggctatt ataataccga aattactgtc      480
aaacagacga tgcttgatgg taatcgtggt aagcttgata tgacctttgc tgaaggtaaa      540
cctgcacggg tgggtgatat taatatcatt ggcaatcagc atttttagcga tgcagatttg      600
attgatgtgc ttgcgattaa ggataataaa atcaatccac tgtctaaagc tgaccgttat      660
actcaagaaa agctgggtgc cagtttagag aatttgcgtg ctaaaatatc caatgcaggg      720
tttgtgcgtt ttgagattaa agatgctaag cttaatatata atgaagataa aaaccgtatc      780
tttgttgaga ttctattgca tgaagggtgag caatatcgct ttggacagac acagtttttg      840
ggtaatttaa cttataactca agcagaactt gaggcactgc ttaaatccaa agcagaagaa      900
gggttttcac aagccatgct tgagcaaaaca acaaacataa tcagtaccaa atttgggtgac      960
gatggctatt attatgctca aatccgtcct gtaacacgca ttaatgatga aagtcgtacg      1020
gttgatgtgg aatattatat tgaccctgta caccctgtct atgtacgccg tattaatttt      1080
acaggtaact ttaagaccca agatgaagta ctccgtcgtg agatgcgaca acttgaagggt      1140
gcgttggcat ctaatcaaaa aatccagctg tctcgtgcac gcttgatgcg gactgggttt      1200
tttaaacatg ttaccggtga tactcgtcca gtacccaact cacctgatca ggttgatgta      1260
aattttgtgg ttgaagaaca accttcagga tcatcaacca tcgcagcagg ctactctcaa      1320
agtgggtggg taacttttca atttgatgtt tctcaaaaata accttatggg tacaggtaag      1380
cacgtcaatg cttcgttttc tcgctctgag acccgtgagg tgtatagttt gggatagacc      1440
aaccataact ttaccgtaaa tggcgtctcg caaagcttga gtggctacta tcgtaaaacc      1500
aagtatgata acaagaacat tagtaattat gtacttgatt cttatgggtg ctcattaagc      1560
tatggatatc caattgatga aaatcaacgc ataagctttg gtctgaatgc tgacaatacc      1620
aagcttcatg gcggtcgttt tatgggcatt agtaatgtca agcagctgat ggcatggtt      1680
ggcaaaattc aagtggataa taatggcatt cctgatttta agcatgatta cacaacctac      1740
aatgccattt tgggggtgaa ttattcaagt ctagatcgcc ctgtatttcc aaccgaaggc      1800
atgtcattct ctgtagtttc gacggttggt ttggtgata aaactcatca aaaagtgggt      1860
tatcaaggca atattctatc cccattttat aaaaaatcag tcttgcgtgg atacgccaaag      1920
ttaggctatg gcaataattt accattttat gaaaaattct atgcaggcgg ctatgggttcg      1980
gttcgtggct atgatcaatc ctctttgggt ccacgctcac aagcctattt gacagctcgt      2040
cgtgggtcaac aaaccacact agggagaggtt gttggtggta atgctttggc aactttcggc      2100
agtgaagctg ttttaccttt gccatttaaa ggtgattgga tagatcaggt gcgtccagtg      2160
atattcattg agggcggtca ggtttttgat acaacaggtg tggataaaca aaccattgat      2220
ttaaccat ttaagacccc acaagcaaca gctgaacaaa atgcaaaaagc agccaatcgc      2280
ccgctactaa cccaagataa acagttgcgt tatagtgtcg gtgttgggtg aacttgggtat      2340
acgcccattg gtcctttatc tattagctat gccaaagcat tgaataaaaa acaaaatgat      2400
cagaccgata cggtagagtt ccagattggt agtgtctttt aa      2442

```

<210> 4

<211> 813

<212> PRT

<213> Bacteria

<400> 4

```

Met Arg Asn Ser Tyr Phe Lys Gly Phe Gln Val Ser Ala Met Thr Met
 1              5              10              15
Ala Val Met Met Val Met Ser Thr His Ala Gln Ala Ala Asp Phe Met
              20              25              30
Ala Asn Asp Ile Ala Ile Thr Gly Leu Gln Arg Val Thr Ile Glu Ser
              35              40              45
Leu Gln Ser Val Leu Pro Phe Arg Leu Gly Gln Val Val Ser Glu Ala
 50              55              60

```

Gln Leu Ala Asp Gly Val Lys Ala Leu Tyr Ala Thr Gly Asn Phe Ser
 65 70 75 80
 Asp Val Gln Val Tyr His Gln Glu Gly Arg Ile Ile Tyr Gln Val Thr
 85 90 95
 Glu Arg Pro Leu Ile Ala Glu Ile Asn Phe Glu Gly Asn Arg Leu Ile
 100 105 110
 Pro Lys Glu Gly Leu Gln Glu Gly Leu Lys Asn Ala Gly Leu Ala Val
 115 120 125
 Gly Gln Pro Leu Lys Gln Ala Thr Val Gln Met Ile Glu Thr Glu Leu
 130 135 140
 Thr Asn Gln Tyr Ile Ser Gln Gly Tyr Tyr Asn Thr Glu Ile Thr Val
 145 150 155 160
 Lys Gln Thr Met Leu Asp Gly Asn Arg Val Lys Leu Asp Met Thr Phe
 165 170 175
 Ala Glu Gly Lys Pro Ala Arg Val Val Asp Ile Asn Ile Ile Gly Asn
 180 185 190
 Gln His Phe Ser Asp Ala Asp Leu Ile Asp Val Leu Ala Ile Lys Asp
 195 200 205
 Asn Lys Ile Asn Pro Leu Ser Lys Ala Asp Arg Tyr Thr Gln Glu Lys
 210 215 220
 Leu Val Thr Ser Leu Glu Asn Leu Arg Ala Lys Tyr Leu Asn Ala Gly
 225 230 235 240
 Phe Val Arg Phe Glu Ile Lys Asp Ala Lys Leu Asn Ile Asn Glu Asp
 245 250 255
 Lys Asn Arg Ile Phe Val Glu Ile Ser Leu His Glu Gly Glu Gln Tyr
 260 265 270
 Arg Phe Gly Gln Thr Gln Phe Leu Gly Asn Leu Thr Tyr Thr Gln Ala
 275 280 285
 Glu Leu Glu Ala Leu Leu Lys Phe Lys Ala Glu Glu Gly Phe Ser Gln
 290 295 300
 Ala Met Leu Glu Gln Thr Thr Asn Asn Ile Ser Thr Lys Phe Gly Asp
 305 310 315 320
 Asp Gly Tyr Tyr Tyr Ala Gln Ile Arg Pro Val Thr Arg Ile Asn Asp
 325 330 335
 Glu Ser Arg Thr Val Asp Val Glu Tyr Tyr Ile Asp Pro Val His Pro
 340 345 350
 Val Tyr Val Arg Arg Ile Asn Phe Thr Gly Asn Phe Lys Thr Gln Asp
 355 360 365
 Glu Val Leu Arg Arg Glu Met Arg Gln Leu Glu Gly Ala Leu Ala Ser
 370 375 380
 Asn Gln Lys Ile Gln Leu Ser Arg Ala Arg Leu Met Arg Thr Gly Phe
 385 390 395 400
 Phe Lys His Val Thr Val Asp Thr Arg Pro Val Pro Asn Ser Pro Asp
 405 410 415
 Gln Val Asp Val Asn Phe Val Val Glu Glu Gln Pro Ser Gly Ser Ser
 420 425 430
 Thr Ile Ala Ala Gly Tyr Ser Gln Ser Gly Gly Val Thr Phe Gln Phe
 435 440 445
 Asp Val Ser Gln Asn Asn Phe Met Gly Thr Gly Lys His Val Asn Ala
 450 455 460
 Ser Phe Ser Arg Ser Glu Thr Arg Glu Val Tyr Ser Leu Gly Met Thr
 465 470 475 480
 Asn Pro Tyr Phe Thr Val Asn Gly Val Ser Gln Ser Leu Ser Gly Tyr
 485 490 495
 Tyr Arg Lys Thr Lys Tyr Asp Asn Lys Asn Ile Ser Asn Tyr Val Leu
 500 505 510
 Asp Ser Tyr Gly Gly Ser Leu Ser Tyr Gly Tyr Pro Ile Asp Glu Asn
 515 520 525

Gln Arg Ile Ser Phe Gly Leu Asn Ala Asp Asn Thr Lys Leu His Gly
 530 535 540
 Gly Arg Phe Met Gly Ile Ser Asn Val Lys Gln Leu Met Ala Asp Gly
 545 550 555 560
 Gly Lys Ile Gln Val Asp Asn Asn Gly Ile Pro Asp Phe Lys His Asp
 565 570 575
 Tyr Thr Thr Tyr Asn Ala Ile Leu Gly Trp Asn Tyr Ser Ser Leu Asp
 580 585 590
 Arg Pro Val Phe Pro Thr Gln Gly Met Ser His Ser Val Asp Leu Thr
 595 600 605
 Val Gly Phe Gly Asp Lys Thr His Gln Lys Val Val Tyr Gln Gly Asn
 610 615 620
 Ile Tyr Arg Pro Phe Ile Lys Lys Ser Val Leu Arg Gly Tyr Ala Lys
 625 630 635 640
 Leu Gly Tyr Gly Asn Asn Leu Pro Phe Tyr Glu Asn Phe Tyr Ala Gly
 645 650 655
 Gly Tyr Gly Ser Val Arg Gly Tyr Asp Gln Ser Ser Leu Gly Pro Arg
 660 665 670
 Ser Gln Ala Tyr Leu Thr Ala Arg Arg Gly Gln Gln Thr Thr Leu Gly
 675 680 685
 Glu Val Val Gly Gly Asn Ala Leu Ala Thr Phe Gly Ser Glu Leu Ile
 690 695 700
 Leu Pro Leu Pro Phe Lys Gly Asp Trp Ile Asp Gln Val Arg Pro Val
 705 710 715 720
 Ile Phe Ile Glu Gly Gly Gln Val Phe Asp Thr Thr Gly Met Asp Lys
 725 730 735
 Gln Thr Ile Asp Leu Thr Gln Phe Lys Asp Pro Gln Ala Thr Ala Glu
 740 745 750
 Gln Asn Ala Lys Ala Ala Asn Arg Pro Leu Leu Thr Gln Asp Lys Gln
 755 760 765
 Leu Arg Tyr Ser Ala Gly Val Gly Ala Thr Trp Tyr Thr Pro Ile Gly
 770 775 780
 Pro Leu Ser Ile Ser Tyr Ala Lys Pro Leu Asn Lys Lys Gln Asn Asp
 785 790 795 800
 Gln Thr Asp Thr Val Gln Phe Gln Ile Gly Ser Val Phe
 805 810

<210> 5
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 5
 actatagggc acgcgtg

17

<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 6
 cctgcgtttg tttgattgag

20

<210> 7
 <211> 61
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 7
 aagggcccaa ttacgcagag gggatccaca ggactacagc gagtgaccat tgaaagctta 60
 c 61

<210> 8
 <211> 67
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 8
 aagggcccaa ttacgcagag ggtcgactta ttaaaagaca ctaccaatct ggaactgtac 60
 cgtatcg 67

<210> 9
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Oligopeptide

<400> 9
 Cys Tyr Ala Lys Pro Leu Asn Lys Lys Gln Asn Asp Gln Thr Asp Thr
 1 5 10 15

<210> 10
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Oligopeptide

<400> 10
 Tyr Leu Thr Ala Arg Arg Gly Gln Gln Thr Thr Leu Gly Glu Val Val
 1 5 10 15
 Cys

SEQUENCE INFORMATION

BASB027 Polynucleotide and Polypeptide Sequences

SEQ ID NO:1

Moraxella catarrhalis BASB027 polynucleotide sequence from strain ATCC 43617

ATGCGTAATTCATATTTTAAAGGTTTTTCAGGTCAGTGCAATGACAATGGCTGTCATGATG
GTAATGTCAACTCATGCACAAGCGGCGGATTTTATGGCAAATGACATTACCATCACAGGA
CTACAGCGAGTGACCATTGAAAGCTTACAAAGCGTGCTGCCGTTTCGCTTGGGTCAAGTG
GTGAGCGAAAACCAAGTTGGCTGATGGTGTCAAAGCACTTTATGCAACAGGCAATTTTTCA
GATGTGCAAGTCTATCATCAAGAAGGGCGTATCATCTATCAGGTAACCGAAAGGCCGTTA
ATCGCTGAGATTAATTTTGAGGGCAATCGCTTAATTCCAAAAGAAGGTCTACAAGAAGGG
CTAAAAAATGCTGGCTTAGCTGTGGGTCAACCACTAAAACAAGCCACAGTACAGATGATC
GAAACCGAGCTTACCAATCAATATATATCACAAAGGCTATTATAATACCGAAATTACTGTC
AAACAGACGATGCTTGATGGTAATCGTGTTAAGCTTGATATGACCTTTGCTGAAGGTAAA
CCTGCACGGGTGGTTGATATTAATATCATTTGGCAATCAGCATTTTAGCGATGCAGATTTG
ATTGATGTGCTTGCATTAAAGGATAATAAATCAATCCACTGTCTAAAGCTGACCGTTAT
ACTCAAGAAAAGCTGGTGACCAGTTTAGAGAATTTGCGTGCTAAATATCTCAATGCAGGG
TTTGTGCGTTTTTGAGATTAAAGATGCTAAGCTTAATATTAATGAAGATAAAAACCGTATC
TTTGTGAGATTTTCATTGCATGAAGGTGAGCAATATCGCTTTGGACAGACACAGTTTTTG
GGTAATTTAACTTATACTCAAGCAGAACTTGAGGCACTGCTTAAATTCAAAGCAGAAGAA
GGGTTTTTCAACAGCCATGCTTGAGCAAAACAACAATATCAGTACCAAATTTGGTGAC
GATGGCTATTATTATGCTCAAATCCGTCCTGTAACACGCATTAATGATGAAAGTCGTACG
GTTGATGTGGAATATTATATTGACCCTGTACACCCTGTCTATGTACGCCGTATTAATTTT
ACAGGTAACTTTAAAGACCCAAGATGAAGTACTCCGTCGTGAGATGCGACAACCTTGAAGGT
GCGTTGGCATCTAATCAAAAAATCCAGCTGTCTCGTGACGCTTGATGCGGACTGGGTTT
TTTAAACATGTTACCGTTGATACTCGTCCAGTACCCAACCTCACCTGATCAGGTTGATGTA
AATTTTGTGGTTGAAGAACAACCTTCAGGATCATCAACCATCGCAGCAGGCTACTCTCAA
AGTGGTGGTGTAACTTTTCAATTTGATGTTTCTCAAAATAACTTTATGGGTACAGGTAAG
CACGTCAATGCTTCGTTTTCTCGCTCTGAGACCCGTGAGGTGTATAGTTTGGGTATGACC
AACCATACTTTACCGTAAATGGCGTCTCGCAAAGCTTGAGTGGCTACTATCGTAAAACC
AAGTATGATAACAAGAACATTAGTAATTATGTACTTGATTCTTATGGTGGCTCATTAAAGC
TATGGATATCCAATTGATGAAAATCAACGCATAAGCTTTGGTCTGAATGCTGACAATACC
AAGCTTCATGGCGGTCGTTTTATGGGCATTAGTAATGTCAAGCAGCTGATGGCAGATGGT
GGCAAAATTCAGTGGATAATAATGGCATTCTGTATTTAAGCATGATTACACAACCTAC
AATGCCATTTTGGGGTGGAATTATTCAAGTCTAGATCGCCCTGTATTTCCAACCCAAGGC
ATGAGTCATTCTGTAGATTTGACGGTTGGTTTTTGGTGATAAACTCATCAAAAAGTGGTT
TATCAAGGCAATATCTATCGCCCATTTATCAAAAAATCAGTCTTGCGTGATACGCCAAG
TTAGGCTATGGCAATAATTTACCATTTTATGAAAATTTCTATGCAGGCGGCTATGGTTCCG
GTTGCTGGCTATGATCAATCCTCTTTGGGTCCACGCTCACAAGCCTATTTGACAGCTCGT
CGTGGTCAACAAACCACACTAGGAGAGGTTGTTGGTGGTAATGCTTTGGCAACTTTCCGGC
AGTGAGCTGATTTTACCTTTGCCATTTAAAGGTGATTGGATAGATCAGGTGCGTCCAGTG
ATATTCATTGAGGGCGGTGAGTTTTTGTATACAACAGGTATGGATAAACAACCAATTGAT
TTAACCCAATTTAAAGACCCACAAGCAACAGCTGAACAAAATGCAAAAGCAGCCAATCGC
CCGCTACTAACCCAAGATAAACAGTTGCGTTATAGTGCTGGTGGTGGTCAACTTGGTAT

ACGCCATTGGTCCTTTATCTATTAGCTATGCCAAGCCATTGAATAAAAAACAAAATGAT
CAGACCGATACGGTACAGTTCCAGATTGGTAGTGTCTTTTAA

SEQ ID NO:2

Moraxella catarrhalis BASB027 polypeptide sequence deduced from the
polynucleotide sequence of SEQ ID NO:1

MRNSYFKGFQVSAMTMAVMMVMSTHAQAADFMANDITITGLQRVTIESLQSVLPFRLGQV
VSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPLIAEINFEGNRLIPKEGLQEG
LKNAGLAVGQPLKQATVQMIETELTNQYISQGYNTEITVKQTMLDGNRVKLDMTFAEGK
PARVVDINIIGNQHFSDADLIDVLAIKDNKINPLSKADRYTQEKLVTSLLENLRAKYLNAG
FVRFEIKDAKLNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAEE
GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPVHPVYVRRINF
TGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGFFKHVTVDRPVPNSPDQVDV
NFVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASFRRSETREVYSLGMT
NPYFTVNGVSQSLSGYYRKT KYDNKNI SNYVLDSYGGSLSYGYPIDENQRISFGLNADNT
KLHGGRFMGISNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSLLDRPVFPTQG
MSHSVLDLTVGFQDKTHQKVYVQGNIRPFIKKSVLRGYAKLGYGNNLPFYENFYAGGYGS
VRGYDQSSSLGPRSQAYLTARRGQQTTLGEVVGGNALATFGSELILPLPFKGDWIDQVRPV
IFIEGGQVFDTTGMDKQTDLTQFKDPQATAEQNAKAANRPLLTQDKQLRYSAGVGATWY
TPIGPLSISYAKPLNKKQNDQTDTVQFQIGSVF

SEQ ID NO:3

Moraxella catarrhalis BASB027 polynucleotide sequence from strain ATCC 43617

ATGCGTAATTCATATTTTAAAGGTTTTTCAGGTCAGTGCAATGACAATGGCTGTCATGATG
GTAATGTCAACTCATGCACAAGCGGCGGATTTTATGGCAAATGACATTACCATCACAGGA
CTACAGCGAGTGACCATTGAAAGCTTACAAAGCGTGCTGCCGTTTTCGCTTGGGTCAAGTG
GTGAGCGAAAACCAGTTGGCTGATGGTGTCAAAGCACTTTATGCAACAGGCAATTTTTCA
GATGTGCAAGTCTATCATCAAGAAGGGCGTATCATCTATCAGGTAACCGAAAGGCCGTTA
ATCGCTGAGATTAATTTTGAGGGCAATCGCTTAATTCCAAAAGAAGGTCTACAAGAAGGG
CTAAAAAATGCTGGCTTAGCTGTGGGTCAACCACTAAAACAAGCCACAGTACAGATGATC
GAAACCGAGCTTACCAATCAATATATATCACAAGGCTATTATAATACCGAAATTACTGTC
AAACAGACGATGCTTGATGGTAATCGTGTTAAGCTTGATATGACCTTTGCTGAAGGTAAA
CCTGCACGGGTGGTTGATATTAATATCATTGGCAATCAGCATTTTAGCGATGCAGATTTG
ATTGATGTGCTTGCGATTAAGGATAATAAAATCAATCCACTGTCTAAAGCTGACCGTTAT
ACTCAAGAAAAGCTGGTGACCAGTTTAGAGAATTTGCGTGCTAAATATCTCAATGCAGGG
TTTGTGCGTTTTGAGATTAAAGATGCTAAGCTTAATATTAATGAAGATAAAAACCGTATC
TTTGTGAGATTTTATTGCATGAAGGTGAGCAATATCGCTTTGGACAGACACAGTTTTTG
GGTAATTTAACTTATACTCAAGCAGAACTTGAGGCACTGCTTAAATTCAAAGCAGAAGAA

GGGTTTTACAAGCCATGCTTGAGCAAACAACAACAATATCAGTACCAAATTTGGTGAC
GATGGCTATTATTATGCTCAAATCCGTCCTGTAACACGCATTAAATGATGAAAGTCGTACG
GTTGATGTGGAATATTATATTGACCTGTACACCCTGTCTATGTACGCCGTATTAATTTT
ACAGGTAACCTTTAAGACCCAAGATGAAGTACTCCGTCGTGAGATGCGACAACCTTGAAGGT
GCGTTGGCATCTAATCAAAAAATCCAGCTGTCTCGTGCACGCTTGATGCGGACTGGGTTT
TTTAAACATGTTACCGTTGATACTCGTCCAGTACCCAACCTCACCTGATCAGGTTGATGTA
AATTTTGTGGTTGAAGAACAACCTTCAGGATCATCAACCATCGCAGCAGGCTACTCTCAA
AGTGGTGGTGTAACTTTTCAATTTGATGTTTCTCAAATAACTTTATGGGTACAGGTAAG
CACGTCAATGCTTCGTTTTCTCGCTCTGAGACCCGTGAGGTGTATAGTTTGGGTATGACC
AACCCTAATCTTTACCGTAAATGGCGTCTCGCAAAGCTTGAGTGGCTACTATCGTAAACC
AAGTATGATAACAAGAACATTAGTAATTATGTAATTGATTCTTATGGTGGCTCATTAGC
TATGGATATCCAATTGATGAAAATCAACGCATAAGCTTTGGTCTGAATGCTGACAATACC
AAGCTTCATGGCGGTTCGTTTTATGGGCATTAGTAATGTCAAGCAGCTGATGGCAGATGGT
GGCAAATTCAGTGGATAATAATGGCATTCTGATTTTAAGCATGATTACACAACCTAC
AATGCCATTTTGGGGTGAATTATTCAAGTCTAGATCGCCCTGTATTTCCAACCCAAGGC
ATGAGTCATTCTGTAGATTTGACGGTTGGTTTTGGTGATAAACTCATCAAAAAGTGGTT
TATCAAGGCAATATCTATCGCCATTTATCAAAAATCAGTCTTGCGTGGATACGCCAAG
TTAGGCTATGGCAATAATTTACCATTTTATGAAAATTTCTATGCAGGCGGCTATGGTTCG
GTTCTGTTGGCTATGATCAATCCTCTTTGGGTCCACGCTCACAAGCCTATTTGACAGCTCGT
CGTGGTCAACAAACCACACTAGGAGAGGTTGTTGGTGGTAATGCTTTGGCAACTTTCGGC
AGTGAGCTGATTTTACCTTTGCCATTTAAAGGTGATTGGATAGATCAGGTGCGTCCAGTG
ATATTCATTGAGGGCGGTTCAGGTTTTGATACAACAGGTATGGATAAAACAAACCATTGAT
TTAACCCAATTTAAAGACCCACAAGCAACAGCTGAACAAAATGCAAAGCAGCCAATCGC
CCGCTACTAACCCAAGATAAACAGTTGCGTTATAGTGCTGGTGTGGTGCAACTTGGTAT
ACGCCCATTTGGTCTTTTATCTATTAGCTATGCCAAGCCATTGAATAAAAAACAAATGAT
CAGACCGATACGGTACAGTTCAGATTGGTAGTGTCTTTTAA

SEQ ID NO:4

Moraxella catarrhalis BASB027 polypeptide sequence deduced from the
polynucleotide sequence of SEQ ID NO:3

MRNSYFKGFQVSAMTMAVMMVMSTHAQAADFMANDITITGLQRVTIESLQSVLPFRLGQV
VSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPLIAEINFEGNRLIPKEGLQEG
LKNAGLAVGQPLKQATVQMIETELTNQYISQGYNTEITVKQTMLDGNRVKLDMTFAEGK
PARVVDINIIGNQHFSADLIDVLAIKDNKINPLSKADRYTQEKLVTSLLENLRAKYLNAG
FVRFEIKDAKLNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAEE
GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPVHPVYVRRINF
TGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGFFKHVTVDTRPVNPSPDQVDV
NFVVEEQPSGSSTIAAGYSQSGGVTFQFDVSQNNFMGTGKHVNASFRRSETREVYSLGMT
NPYFTVNGVSQSLSGYYRKT KYDNKNISNYVLDSYGGSLSYGYPIDENQRISFGLNADNT
KLHGGFRMGISNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSLLDRPVFPQTQ
MSHSVDLTVGFGDKTHQKVYQGNIRPFIKKSVLRGYAKLGYGNLFPYENFYAGGYGS
VRGYDQSSSLGPRSQAYLTARRGQQTTLGEVVGGNALATFGSELILPLPKGDWIDQVRPV
IFIEGGQVFDTTGMDKQTDILTQFKDPQATAEQNAKAANRPLLTQDKQLRYSAGVGATWY

TPIGPLSISYAKPLNKKQNDQTDTVQFQIGSVF

SEQ ID NO:5

ACT ATA GGG CAC GCG TG

SEQ ID NO:6

CCT GCG TTT GTT TGA TTG AG

SEQ ID NO:7

AAG GGC CCA ATT ACG CAG AGG GGA TCC ACA GGA CTA CAG CGA GTG
ACC ATT GAA AGC TTA C

SEQ ID NO:8

AAG GGC CCA ATT ACG CAG AGG GTC GAC TTA TTA AAA GAC ACT ACC
AAT CTG GAA CTG TAC CGT ATC G

SEQ ID NO:9

CYAKPLNKKQNDQTD

SEQ ID NO:10

YLTARRGQQTTLGEVVC

13/26

Figure 2 : Alignment of the BASB027 polynucleotide sequences.

Identity to SeqID No:1 is indicated by a dot.

```

          *           20           *           40           *
Seqid1 : ATGCGTAATTCATATTTTAAAGGTTTTCAGGTCAGTGCAATGACAATGGC : 50
Seqid3 : ..... : 50

          60           *           80           *           100
Seqid1 : TGTCATGATGGTAATGTCAACTCATGCACAAGCGGCGGATTTTATGGCAA : 100
Seqid3 : ..... : 100

          *           120           *           140           *
Seqid1 : ATGACATTACCATCACAGGACTACAGCGAGTGACCATTGAAAGCTTACAA : 150
Seqid3 : .....G..... : 150

          160           *           180           *           200
Seqid1 : AGCGTGCTGCCGTTTCGCTTGGGTCAAGTGGTGAGCGAAAACCGATTGGC : 200
Seqid3 : .....GCA..... : 200

          *           220           *           240           *
Seqid1 : TGATGGTGTCAAAGCACTTTATGCAACAGGCAATTTTTCAGATGTGCAAG : 250
Seqid3 : ..... : 250

          260           *           280           *           300
Seqid1 : TCTATCATCAAGAAGGGCGTATCATCTATCAGGTAACCGAAAGGCCGTTA : 300
Seqid3 : ..... : 300

          *           320           *           340           *
Seqid1 : ATCGCTGAGATTAATTTTGAGGGCAATCGCTTAATTCCAAAGAAGGTCT : 350
Seqid3 : ..... : 350

```

14 / 26

360 * 380 * 400
Seqid1 : ACAAGAAGGGCTAAAAAATGCTGGCTTAGCTGTGGGTCAACCACTAAAAC : 400
Seqid3 : : 400

* 420 * 440 *
Seqid1 : AAGCCACAGTACAGATGATCGAAACCGAGCTTACCAATCAATATATATCA : 450
Seqid3 : : 450

460 * 480 * 500
Seqid1 : CAAGGCTATTATAATACCGAAATTACTGTCAAACAGACGATGCTTGATGG : 500
Seqid3 : : 500

* 520 * 540 *
Seqid1 : TAATCGTGTTAAGCTTGATATGACCTTTGCTGAAGGTAAACCTGCACGGG : 550
Seqid3 : : 550

560 * 580 * 600
Seqid1 : TGGTTGATATTAATATCATTGGCAATCAGCATTTTAGCGATGCAGATTTG : 600
Seqid3 : : 600

* 620 * 640 *
Seqid1 : ATTGATGTGCTTGCGATTAAGGATAATAAAATCAATCCACTGTCTAAAGC : 650
Seqid3 : : 650

660 * 680 * 700
Seqid1 : TGACCGTTTACTCAAGAAAAGCTGGTGACCAGTTTAGAGAATTTGCGTG : 700
Seqid3 : : 700

* 720 * 740 *
Seqid1 : CTAAATATCTCAATGCAGGGTTTGTGCGTTTTGAGATTAAAGATGCTAAG : 750

15/26

Seqid3 : : 750

760 * 780 * 800
Seqid1 : CTTAATATTAATGAAGATAAAAACCGTATCTTTGTTGAGATTTTCATTGCA : 800
Seqid3 : : 800

* 820 * 840 *
Seqid1 : TGAAGGTGAGCAATATCGCTTTGGACAGACACAGTTTTTGGGTAATTTAA : 850
Seqid3 : : 850

860 * 880 * 900
Seqid1 : CTTATACTCAAGCAGAACTTGAGGCACTGCTTAAATTCAAAGCAGAAGAA : 900
Seqid3 : : 900

* 920 * 940 *
Seqid1 : GGGTTTTTACAAGCCATGCTTGAGCAAACAACAATATCAGTACCAA : 950
Seqid3 : : 950

960 * 980 * 1000
Seqid1 : ATTTGGTGACGATGGCTATTATTATGCTCAAATCCGTCCTGTAACACGCA : 1000
Seqid3 : : 1000

* 1020 * 1040 *
Seqid1 : TTAATGATGAAAGTCGTACGGTTGATGTGGAATATTATATTGACCCTGTA : 1050
Seqid3 : : 1050

1060 * 1080 * 1100
Seqid1 : CACCCTGTCTATGTACGCCGTATTAATTTTACAGGTAACTTTAAGACCCA : 1100
Seqid3 : : 1100

16/26

 * 1120 * 1140 *

Seqid1 : AGATGAAGTACTCCGTCGTGAGATGCGACAACCTGAAGGTGCGTTGGCAT : 1150

Seqid3 : : 1150

 1160 * 1180 * 1200

Seqid1 : CTAATCAAAAAATCCAGCTGTCTCGTGCACGCTTGATGCGGACTGGGTTT : 1200

Seqid3 : : 1200

 * 1220 * 1240 *

Seqid1 : TTTAAACATGTTACCGTTGATACTCGTCCAGTACCCAACTCACCTGATCA : 1250

Seqid3 : : 1250

 1260 * 1280 * 1300

Seqid1 : GGTGATGTAAATTTTGTGGTTGAAGAACAACCTTCAGGATCATCAACCA : 1300

Seqid3 : : 1300

 * 1320 * 1340 *

Seqid1 : TCGCAGCAGGCTACTCTCAAAGTGGTGGTGTAACTTTTCAATTTGATGTT : 1350

Seqid3 : : 1350

 1360 * 1380 * 1400

Seqid1 : TCTCAAATAACTTTATGGGTACAGGTAAGCACGTCAATGCTTCGTTTTTC : 1400

Seqid3 : : 1400

 * 1420 * 1440 *

Seqid1 : TCGCTCTGAGACCCGTGAGGTGTATAGTTTGGGTATGACCAACCCATACT : 1450

Seqid3 : : 1450

 1460 * 1480 * 1500

Seqid1 : TTACCGTAAATGGCGTCTCGCAAAGCTTGAGTGGCTACTATCGTAAACC : 1500

Seqid3 : : 1500

17/26

* 1520 * 1540 *
Seqid1 : AAGTATGATAACAAGAACATTAGTAATTATGTACTTGATTCTTATGGTGG : 1550
Seqid3 : : 1550

1560 * 1580 * 1600
Seqid1 : CTCATTAAGCTATGGATATCCAATTGATGAAAATCAACGCATAAGCTTTG : 1600
Seqid3 : : 1600

* 1620 * 1640 *
Seqid1 : GTCTGAATGCTGACAATACCAAGCTTCATGGCGGTCGTTTTATGGGCATT : 1650
Seqid3 : : 1650

1660 * 1680 * 1700
Seqid1 : AGTAATGTCAAGCAGCTGATGGCAGATGGTGGCAAAATTCAAGTGGATAA : 1700
Seqid3 : : 1700

* 1720 * 1740 *
Seqid1 : TAATGGCATTCTGATTTTAAGCATGATTACACAACCTACAATGCCATTT : 1750
Seqid3 : : 1750

1760 * 1780 * 1800
Seqid1 : TGGGGTGAATTATTCAAGTCTAGATCGCCCTGTATTTCCAACCCAAGGC : 1800
Seqid3 : : 1800

* 1820 * 1840 *
Seqid1 : ATGAGTCATTCTGTAGATTTGACGGTTGGTTTTGGTGATAAACTCATCA : 1850
Seqid3 : : 1850

1860 * 1880 * 1900
Seqid1 : AAAAGTGGTTTATCAAGGCAATATCTATCGCCCATTTATCAAAAAATCAG : 1900

18/26

```
Seqid3 : ..... : 1900
```

```

          *          1920          *          1940          *
Seqid1  : TCTTGCGTGGATACGCCAAGTTAGGCTATGGCAATAATTTACCATTTTAT : 1950
Seqid3  : ..... : 1950

```

```

          1960          *          1980          *          2000
Seqid1 : GAAAATTTCTATGCAGGCGGCTATGGTTCGGTTCGTGGCTATGATCAATC : 2000
Seqid3 : ..... : 2000

```

```

          *          2020          *          2040          *
Seqid1  : CTCTTTGGGTCCACGCTCACAAAGCCTATTTGACAGCTCGTCGTGGTCAAC : 2050
Seqid3  : ..... : 2050

```

```

                2060          *          2080          *          2100
Seqid1  : AAACCACACTAGGAGAGGTTGTTGGTGGTAATGCTTTGGCAACTTTCGGC : 2100
Seqid3  : ..... : 2100

```

```

                *          2120                *          2140                *
Seqid1  : AGTGAGCTGATTTTACCTTTGCCATTTAAAGGTGATTGGATAGATCAGGT : 2150
Seqid3  : ..... : 2150

```

```

                2160          *          2180          *          2200
Seqid1  :  GCGTCCAGTGATATTCATTGAGGGCGGTCAGGTTTTTGATACAACAGGTA  : 2200
Seqid3  :  ..... : 2200

```

```

          *          2220          *          2240          *
Seqid1  : TGGATAAACAAACCATTGATTTAACCCAATTTAAAGACCCACAAGCAACA : 2250
Seqid3  : ..... : 2250

```

19/26

2260 * 2280 * 2300
Seqid1 : GCTGAACAAAATGCAAAAGCAGCCACTCGCCCGCTACTAACCCAAGATAA : 2300
Seqid3 : : 2300

* 2320 * 2340 *
Seqid1 : ACAGTTGCGTTATAGTGCTGGTGTGGTGCAACTTGGTATACGCCCCATTG : 2350
Seqid3 : : 2350

2360 * 2380 * 2400
Seqid1 : GTCCTTTATCTATTAGCTATGCCAAGCCATTGAATAAAAAACAAAATGAT : 2400
Seqid3 : : 2400

* 2420 * 2440
Seqid1 : CAGACCGATACGGTACAGTTCCAGATTGGTAGTGTCTTTTAA : 2442
Seqid3 : : 2442

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151
2152
2153
2154
2155

20/26

Figure 3 : Alignment of the BASB027 polypeptide sequences.

Identity to SeqID No:2 is indicated by a dot.

```

                *           20           *           40           *
Seqid2 : MRNSYFKGFQVSAMTMVMMVMSTHAQAADFMANDITITGLQRTIESLQ : 50
Seqid4 : .....A..... : 50

                60           *           80           *           100
Seqid2 : SVLPFRLGQVVSENQLADGVKALYATGNFSDVQVYHQEGRIIYQVTERPL : 100
Seqid4 : .....A..... : 100

                *           120           *           140           *
Seqid2 : IAEINFEGNRLIPKEGLQEGLKNAGLAVGQPLKQATVQMIETELTNQYIS : 150
Seqid4 : ..... : 150

                160           *           180           *           200
Seqid2 : QGYNTEITVKQTMLDGNRVKLDMTFAEGKPARVVDINIIGNQHFSDADL : 200
Seqid4 : ..... : 200

                *           220           *           240           *
Seqid2 : IDVLAIKDNKINPLSKADRYTQEKLVTSLENLRAKYLNAGFVRFEIKDAK : 250
Seqid4 : ..... : 250

                260           *           280           *           300
Seqid2 : LNINEDKNRIFVEISLHEGEQYRFGQTQFLGNLTYTQAELEALLKFKAEE : 300
Seqid4 : ..... : 300

                *           320           *           340           *
Seqid2 : GFSQAMLEQTTNNISTKFGDDGYYYAQIRPVTRINDESRTVDVEYYIDPV : 350
Seqid4 : ..... : 350
```

21/26

360 * 380 * 400
Seqid2 : HPVYVRRINFTGNFKTQDEVLRREMRQLEGALASNQKIQLSRARLMRTGF : 400
Seqid4 : : 400

* 420 * 440 *
Seqid2 : FKHVTVDTRPVNPSPDQVDVNFVVEEQPSGSSTIAAGYSQSGGVTFQFDV : 450
Seqid4 : : 450

460 * 480 * 500
Seqid2 : SQNNFMGTGKHVNASFRRSETREVYSLGMTNPYFTVNGVSQSLSGYYRKT : 500
Seqid4 : : 500

* 520 * 540 *
Seqid2 : KYDNKNISNYVLDSYGGSLSYGYPIDENQRISFGLNADNTKLHGGRFMGI : 550
Seqid4 : : 550

560 * 580 * 600
Seqid2 : SNVKQLMADGGKIQVDNNGIPDFKHDTTYNAILGWNYSLLDRPVFPTQG : 600
Seqid4 : : 600

* 620 * 640 *
Seqid2 : MSHSVDLTVGFGDKTHQKVYQGNIIYRPFIKKSVLRGYAKLGYGNNLPFY : 650
Seqid4 : : 650

660 * 680 * 700
Seqid2 : ENFYAGGYGSVRGYDQSSLGPRSQAYLTARRGQOTTLGEVVGGNALATFG : 700
Seqid4 : : 700

* 720 * 740 *
Seqid2 : SELILPLPFKGDWIDQVRPVIFIEGGQVFDTTGMDKQTIDLTQFKDPQAT : 750

22/26

Seqid4 : : 750

760

*

780

*

800

Seqid2 : AEQNAKAAANRPLLTDKQLRYSAGVGATWYTPIGPLSISYAKPLNKKQNE : 800

Seqid4 : : 800

*

Seqid2 : QTDTVQFQIGSVF : 813

Seqid4 : : 813

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040
1041
1042
1043
1044
1045
1046
1047
1048
1049
1050
1051
1052
1053
1054
1055
1056
1057
1058
1059
1060
1061
1062
1063
1064
1065
1066
1067
1068
1069
1070
1071
1072
1073
1074
1075
1076
1077
1078
1079
1080
1081
1082
1083
1084
1085
1086
1087
1088
1089
1090
1091
1092
1093
1094
1095
1096
1097
1098
1099
1100
1101
1102
1103
1104
1105
1106
1107
1108
1109
1110
1111
1112
1113
1114
1115
1116
1117
1118
1119
1120
1121
1122
1123
1124
1125
1126
1127
1128
1129
1130
1131
1132
1133
1134
1135
1136
1137
1138
1139
1140
1141
1142
1143
1144
1145
1146
1147
1148
1149
1150
1151
1152
1153
1154
1155
1156
1157
1158
1159
1160
1161
1162
1163
1164
1165
1166
1167
1168
1169
1170
1171
1172
1173
1174
1175
1176
1177
1178
1179
1180
1181
1182
1183
1184
1185
1186
1187
1188
1189
1190
1191
1192
1193
1194
1195
1196
1197
1198
1199
1200
1201
1202
1203
1204
1205
1206
1207
1208
1209
1210
1211
1212
1213
1214
1215
1216
1217
1218
1219
1220
1221
1222
1223
1224
1225
1226
1227
1228
1229
1230
1231
1232
1233
1234
1235
1236
1237
1238
1239
1240
1241
1242
1243
1244
1245
1246
1247
1248
1249
1250
1251
1252
1253
1254
1255
1256
1257
1258
1259
1260
1261
1262
1263
1264
1265
1266
1267
1268
1269
1270
1271
1272
1273
1274
1275
1276
1277
1278
1279
1280
1281
1282
1283
1284
1285
1286
1287
1288
1289
1290
1291
1292
1293
1294
1295
1296
1297
1298
1299
1300
1301
1302
1303
1304
1305
1306
1307
1308
1309
1310
1311
1312
1313
1314
1315
1316
1317
1318
1319
1320
1321
1322
1323
1324
1325
1326
1327
1328
1329
1330
1331
1332
1333
1334
1335
1336
1337
1338
1339
1340
1341
1342
1343
1344
1345
1346
1347
1348
1349
1350
1351
1352
1353
1354
1355
1356
1357
1358
1359
1360
1361
1362
1363
1364
1365
1366
1367
1368
1369
1370
1371
1372
1373
1374
1375
1376
1377
1378
1379
1380
1381
1382
1383
1384
1385
1386
1387
1388
1389
1390
1391
1392
1393
1394
1395
1396
1397
1398
1399
1400
1401
1402
1403
1404
1405
1406
1407
1408
1409
1410
1411
1412
1413
1414
1415
1416
1417
1418
1419
1420
1421
1422
1423
1424
1425
1426
1427
1428
1429
1430
1431
1432
1433
1434
1435
1436
1437
1438
1439
1440
1441
1442
1443
1444
1445
1446
1447
1448
1449
1450
1451
1452
1453
1454
1455
1456
1457
1458
1459
1460
1461
1462
1463
1464
1465
1466
1467
1468
1469
1470
1471
1472
1473
1474
1475
1476
1477
1478
1479
1480
1481
1482
1483
1484
1485
1486
1487
1488
1489
1490
1491
1492
1493
1494
1495
1496
1497
1498
1499
1500
1501
1502
1503
1504
1505
1506
1507
1508
1509
1510
1511
1512
1513
1514
1515
1516
1517
1518
1519
1520
1521
1522
1523
1524
1525
1526
1527
1528
1529
1530
1531
1532
1533
1534
1535
1536
1537
1538
1539
1540
1541
1542
1543
1544
1545
1546
1547
1548
1549
1550
1551
1552
1553
1554
1555
1556
1557
1558
1559
1560
1561
1562
1563
1564
1565
1566
1567
1568
1569
1570
1571
1572
1573
1574
1575
1576
1577
1578
1579
1580
1581
1582
1583
1584
1585
1586
1587
1588
1589
1590
1591
1592
1593
1594
1595
1596
1597
1598
1599
1600
1601
1602
1603
1604
1605
1606
1607
1608
1609
1610
1611
1612
1613
1614
1615
1616
1617
1618
1619
1620
1621
1622
1623
1624
1625
1626
1627
1628
1629
1630
1631
1632
1633
1634
1635
1636
1637
1638
1639
1640
1641
1642
1643
1644
1645
1646
1647
1648
1649
1650
1651
1652
1653
1654
1655
1656
1657
1658
1659
1660
1661
1662
1663
1664
1665
1666
1667
1668
1669
1670
1671
1672
1673
1674
1675
1676
1677
1678
1679
1680
1681
1682
1683
1684
1685
1686
1687
1688
1689
1690
1691
1692
1693
1694
1695
1696
1697
1698
1699
1700
1701
1702
1703
1704
1705
1706
1707
1708
1709
1710
1711
1712
1713
1714
1715
1716
1717
1718
1719
1720
1721
1722
1723
1724
1725
1726
1727
1728
1729
1730
1731
1732
1733
1734
1735
1736
1737
1738
1739
1740
1741
1742
1743
1744
1745
1746
1747
1748
1749
1750
1751
1752
1753
1754
1755
1756
1757
1758
1759
1760
1761
1762
1763
1764
1765
1766
1767
1768
1769
1770
1771
1772
1773
1774
1775
1776
1777
1778
1779
1780
1781
1782
1783
1784
1785
1786
1787
1788
1789
1790
1791
1792
1793
1794
1795
1796
1797
1798
1799
1800
1801
1802
1803
1804
1805
1806
1807
1808
1809
1810
1811
1812
1813
1814
1815
1816
1817
1818
1819
1820
1821
1822
1823
1824
1825
1826
1827
1828
1829
1830
1831
1832
1833
1834
1835
1836
1837
1838
1839
1840
1841
1842
1843
1844
1845
1846
1847
1848
1849
1850
1851
1852
1853
1854
1855
1856
1857
1858
1859
1860
1861
1862
1863
1864
1865
1866
1867
1868
1869
1870
1871
1872
1873
1874
1875
1876
1877
1878
1879
1880
1881
1882
1883
1884
1885
1886
1887
1888
1889
1890
1891
1892
1893
1894
1895
1896
1897
1898
1899
1900
1901
1902
1903
1904
1905
1906
1907
1908
1909
1910
1911
1912
1913
1914
1915
1916
1917
1918
1919
1920
1921
1922
1923
1924
1925
1926
1927
1928
1929
1930
1931
1932
1933
1934
1935
1936
1937
1938
1939
1940
1941
1942
1943
1944
1945
1946
1947
1948
1949
1950
1951
1952
1953
1954
1955
1956
1957
1958
1959
1960
1961
1962
1963
1964
1965
1966
1967
1968
1969
1970
1971
1972
1973
1974
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
2024
2025
2026
2027
2028
2029
2030
2031
2032
2033
2034
2035
2036
2037
2038
2039
2040
2041
2042
2043
2044
2045
2046
2047
2048
2049
2050
2051
2052
2053
2054
2055
2056
2057
2058
2059
2060
2061
2062
2063
2064
2065
2066
2067
2068
2069
2070
2071
2072
2073
2074
2075
2076
2077
2078
2079
2080
2081
2082
2083
2084
2085
2086
2087
2088
2089
2090
2091
2092
2093
2094
2095
2096
2097
2098
2099
2100
2101
2102
2103
2104
2105
2106
2107
2108
2109
2110
2111
2112
2113
2114
2115
2116
2117
2118
2119
2120
2121
2122
2123
2124
2125
2126
2127
2128
2129
2130
2131
2132
2133
2134
2135
2136
2137
2138
2139
2140
2141
2142
2143
2144
2145
2146
2147
2148
2149
2150
2151

23/26

Figure 4: Coomassie stained SDS-PAGE of purified BASB027 protein.

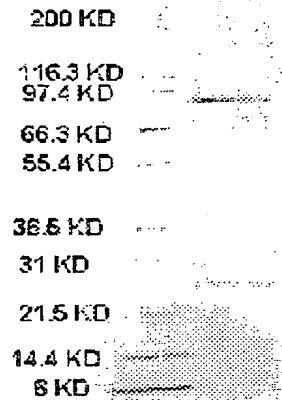
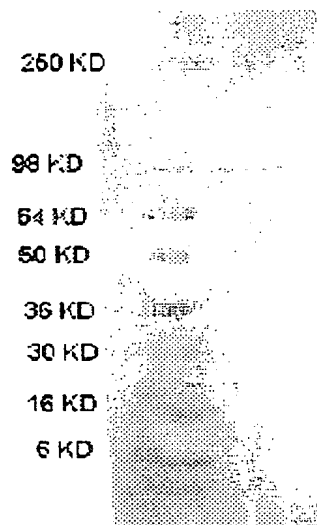
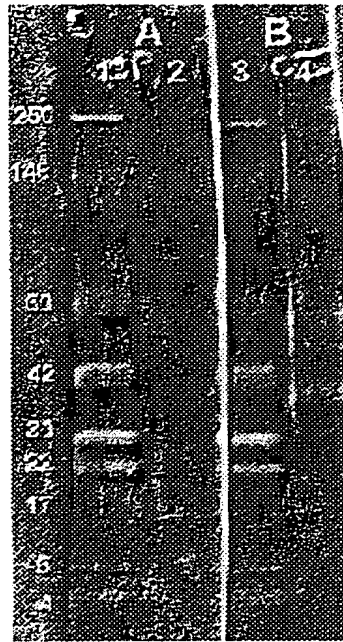


Figure 5: Western blot with tera-His antibody of purified BASB027 protein.



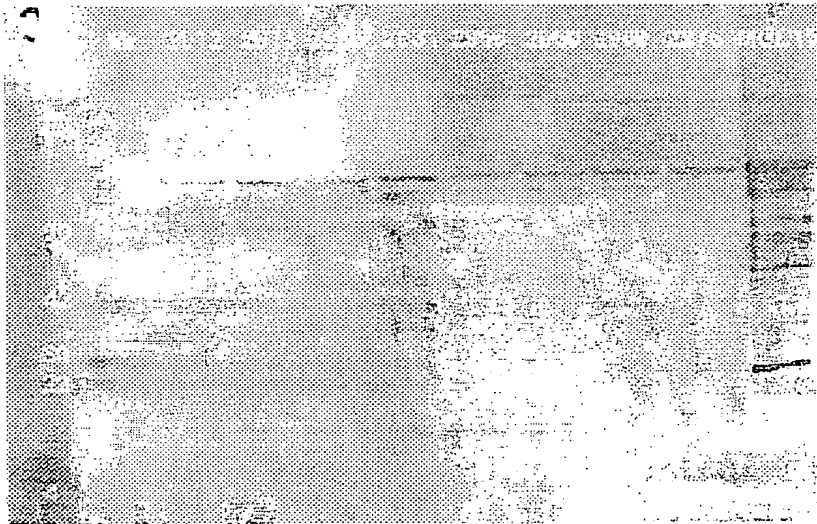
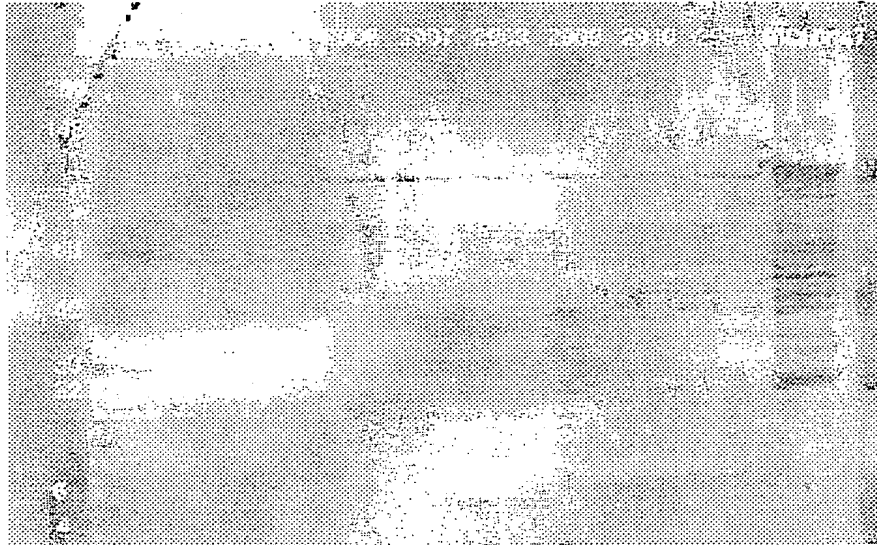
24/26

Figure 6: Western blot of purified BASB027 protein with the corresponding anti-recombinant protein sera. Panel A: pre-immune serum. Panel B: immune serum.



25/26

Figure 7: Western blot of whole cell lysates of 16 strains of *M. catarrhalis* using pooled sera against the BASB027 protein (sera was diluted 1:2000).



26/26

Figure 8: Western blot of purified recombinant BASB027 with corresponding anti-peptide sera. Lanes 2 and 3 non immune sera. Lanes 1 and 4 immune sera.

